

Sequence Listing

<110> ASHKENAZI, AVI J
BOTSTEIN, DAVID
DODGE, KELLY H.
GURNEY, AUSTIN L.
KIM, KYUNG JIN
LAWRENCE, DAVID A.
PITTI, ROBERT
ROY, MARGARET A
TUMAS, DANIEL B
WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289
<141> 1998-09-18

<150> US 60/059,288
<151> 1997-09-18

<150> US 60/094,640
<151> 1998-07-30

<160> 18

<210> 1
<211> 300
<212> PRT
<213> Homo sapiens

<400> 1
Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val
1 5 10 15

Leu Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val
20 25 30

Ala Glu Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu
35 40 45

Arg Leu Val Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg
50 55 60

Pro Cys Arg Arg Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro
65 70 75

Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr
80 85 90

Cys Asn Val Leu Cys Gly Glu Arg Glu Glu Ala Arg Ala Cys
95 100 105

His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly Phe Phe
110 115 120

Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro Gly
125 130 135

Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys
140 145 150

Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser
155 160 165

Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala
170 175 180

Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser
185 190 195

Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu
200 205 210

Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser
215 220 225

Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
230 235 240

Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu
245 250 255

Lys Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly
260 265 270

Ala Leu Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met
275 280 285

Pro Gly Leu Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
290 295 300

<210> 2
<211> 1114
<212> DNA
<213> Homo sapiens

<220>
<221> Unsure
<222> 1090

<223> Unknown base

<400> 2

tccgcaggcg gaccgggggc aaaggaggtg gcatgtcggt caggcacagc 50
agggtcctgt gtccgcgctg agccgcgctc tccctgctcc agcaaggacc 100
atgagggcgc tggagggggcc aggccctgtcg ctgctgtgcc tggtgttggc 150
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200
ccacacctacc cttggcggac gcagagacag gggagcggct ggtgtgcgcc 250
cagtgcaccc caggcacctt tgtgcagcgg ccgtgccgccc gagacagccc 300
cacgacgtgt ggcccggttc caccgcgcac ctacacgcag ttctggaact 350
acctggagcg ctgcccgtac tgcaacgtcc tctgccccca gcgtgaggag 400
gagggcacggg cttgccacgc cacccacaac cgtgcctgcc gctgccgcac 450
cggttcttc ggcgcacgctg gtttctgttt ggagcacgca tcgtgtccac 500
ctggtgccgg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550
cagccgtgcc ccccaggcac cttctcagcc agcagctcca gctcagagca 600
gtgccagccc caccgcaact gcacggccct ggccctggcc ctcaatgtgc 650
caggtcttc ctccccatgac accctgtgca ccagctgcac tggcttcccc 700
ctcagcacca gggtaccagg agctgaggag tgtgagcgtg ccgtcatcga 750
ctttgtggct ttccaggaca tctccatcaa gaggctgcag cggctgctgc 800
aggccctcga ggccccggag ggctggggtc cgacaccaag ggccggccgc 850
gcggccttgc agctgaagct gcgtcggcggt ctcacggagc tcctggggc 900
gcaggacggg gcgcgtctgg tgccggctgt gcagggcgctg cgcgtggccca 950
ggatgcccgg gctggagcgg agcgtccgtg agcgcttctt ccctgtgcac 1000
tgatcctggc ccccttttat ttattctaca tccttggcac cccacttgca 1050
ctgaaaagagg cttttttta aatagaagaa atgaggttt taaaaaaaaa 1100
aaaaaaaaaa aaaa 1114

<210> 3

<211> 491

<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 62, 73, 86, 98
<223> unknown base

<400> 3
gccgagacag ccccacgacg tgtggcccg gtccaccgcg ccactacacg 50
cagttctgga antaactgga gcnctgccgc tactgnaacg tcctctgnng 100
ggagcgtgag gaggaggcac gggcttgcca cgccacccac aaccgtgcct 150
gccgctgcgg caccggcttc ttgcgcacg ctggtttctg cttggagcac 200
gcatcgtgtc cacctgggtgc cggcgtgatt gccccggca cccccagcca 250
gaacacgcag tgccttagccg tgccccccag gcaccttctc agccagcaga 300
tccagctcag agcagtgcca gccccaccgc aactgcacgg ccctgggcct 350
ggccctcaat gtgccaggct cttcctccca tgacaccctg tgcaccagct 400
gcactggctt ccccctcagc accagggtac caggagctga ggagtgtgag 450
cgtgccgtca tcgactttgt ggcttccag gacatctcca t 491

<210> 4
<211> 73
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 4
gccgagacag ccccacgacg tgtggcccg gtccaccgcg ccactacacg 50
cattctggaa ctacctggag cgc 73

<210> 5
<211> 271
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

<223> unknown base

<400> 5
gccgagacag ccccacgacg tgtggccgt gtccaccgcg cnactacacg 50

cagttctgga antaactgga gcncgtccgc tactgnaacg tcctctgnng 100

ggagcntgag gaggaggcan gngcttgcca cgccacccac aaccgcgcct 150

gcngctgcag caccggnttc ttgcgcacg ctgnnttctg cttggagcac 200

gcatcgtgtc cacctggtgn cggcgtgatt gcncgggca cccccagcca 250

gaacacgcat gcaaagccgt g 271

<210> 6

<211> 201

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 182

<223> unknown base

<400> 6
gcagttctgg aactacctgg agcgctgccc ctactgcaac gtcctctgcg 50

gggagcgtga ggaggaggca cgggcttgcc acgccaccca caaccgtgcc 100

tgccgctgcc gcaccggctt ctgcgcac gctggttct gttggagca 150

cgcatcgtgt ccacctggtg cggcgtgat tnccccggc acccccagcc 200

a 201

<210> 7

<211> 277

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>
<221> unsure
<222> 142
<223> unknown base

<400> 7
gagggggccc caggagtggt ggccggaggt gtggcagggg tcaggttgtct 50
ggtcccagcc ttgcaccctg agctaggaca ccagttcccc tgaccctgtt 100
cttccctcct ggctgcaggc accccccagcc agaacacgca gnccagccgt 150
gcccccagg caccttctca gccagcagct ccagtcaga gcagtgccag 200
ccccacccgca actgcacggc cctgggcctg gcccctaatt tgccaggctc 250
ttcctccat gacaccctgt gcaccag 277

<210> 8
<211> 199
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 8
gcacatcggtc cacctgggtgc cggcgtgatt gccccggca ccccccagcca 50
gaacacgcag gccttagccgt gccccccagg caccttctca gccagcagct 100
ccagtcaga gcagtgccag cccacccgca actgcacggc cctgggcctg 150
gcccctaatt tgccaggctc ttcctccat gacaccctgt gcaccagct 199

<210> 9
<211> 226
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 4, 9, 12, 165
<223> unknown base

<400> 9
agcngtgcnnc cncaggcacc ttctcagcca gcagttccag ctcagagcag 50

tgccagcccc accgcaactg cacggccctg ggcctggccc tcaatgtgcc 100
aggctttcc tcccatgaca cgctgtcac cagctgcact ggcttcccc 150
tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcatcgac 200
tttgtggctt tccaggacat ctccat 226

<210> 10
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> Unsure
<222> 1-283
<223> Unknown organism

<220>
<221> unsure
<222> 27, 64, 140
<223> unknown base

<400> 10
cttgtccacc tggtgccggc gtgattnccc gggcacccccc agccagaaca 50
cgcagtgcaca gcncntcccc caggcacacctt ctcagccagc agctccagct 100
cagagcagtgc ctagccccac cgcaactgca acgcctgggn ctggccctca 150
atgtgccagg ctcttcctcc catgacacccc tgtgcaccag ctgcactggc 200
ttccccctca gcaccagggt accaggagct gaggagtgtg agcgtgcgt 250
catcgacttt gtggctttcc aggacatctc cat 283

<210> 11
<211> 21
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 11
cacgctggtt tctgcttggaa g 21

<210> 12
<211> 22
<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 12
agctggtgca cagggtgtca tg 22

<210> 13
<211> 53
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<400> 13
cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag 50
ccc 53

<210> 14
<211> 24
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<400> 14
acacgatgcg tgctccaagc agaa 24

<210> 15
<211> 17
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<400> 15
cttcttcgcg cacgctg 17

<210> 16
<211> 16
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<400> 16
atcacgccgg caccag 16

<210> 17
<211> 461
<212> PRT
<213> Homo sapiens

<400> 17

Met	Ala	Pro	Val	Ala	Val	Trp	Ala	Ala	Leu	Ala	Val	Gly	Leu	Gl
1					5						10			15

Leu Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr

		20							25				30
--	--	----	--	--	--	--	--	--	----	--	--	--	----

Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr

		35					40					45
--	--	----	--	--	--	--	----	--	--	--	--	----

Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly

		50				55					60
--	--	----	--	--	--	----	--	--	--	--	----

Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys

		65				70					75
--	--	----	--	--	--	----	--	--	--	--	----

Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val

		80			85					90
--	--	----	--	--	----	--	--	--	--	----

Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val

		95			100					105
--	--	----	--	--	-----	--	--	--	--	-----

Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys

		110			115					120
--	--	-----	--	--	-----	--	--	--	--	-----

Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg

		125			130					135
--	--	-----	--	--	-----	--	--	--	--	-----

Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala

		140			145					150
--	--	-----	--	--	-----	--	--	--	--	-----

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala

		155			160					165
--	--	-----	--	--	-----	--	--	--	--	-----

Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg

		170			175					180
--	--	-----	--	--	-----	--	--	--	--	-----

Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser

		185			190					195
--	--	-----	--	--	-----	--	--	--	--	-----

Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala

		200			205					210
--	--	-----	--	--	-----	--	--	--	--	-----

Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
215 220 225

His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr
245 250 255

Gly Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala
260 265 270

Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr
275 280 285

Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val
290 295 300

Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu
305 310 315

Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser
320 325 330

Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg
335 340 345

Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu
350 355 360

Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His
365 370 375

Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser
380 385 390

Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met
395 400 405

Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln
410 415 420

Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
425 430 435

Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro
440 445 450

Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
455 460

<210> 18
<211> 293
<212> PRT
<213> Homo sapiens

<400> 18
Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
1 5 10 15

Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
20 25 30

Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
35 40 45

Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
50 55 60

Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Asp Ser Trp His
65 70 75

Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
80 85 90

Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
95 100 105

Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
110 115 120

His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
125 130 135

Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
140 145 150

Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
155 160 165

Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
170 175 180

His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
185 190 195

Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
200 205 210

Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
215 220 225

Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile
260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
275 280 285

Gly His Ala Asn Leu Thr Phe Glu
290